

**RAW SEQUENCE LISTING
PATENT APPLICATION US/09/479,240**DATE: 02/01/2000
TIME: 23:28:19**INPUT SET: S34590.raw**

This Raw Listing contains the General
Information Section and up to the first 5 pages.

1 SEQUENCE LISTING
2
3 (1) General Information:
4
5 (i) APPLICANT: KLEIN, Michel H
6 DU, Run-Pan
7 EWASYSHYN, Mary E
8
9 (ii) TITLE OF INVENTION: INFECTATION DETECTION METHOD USING
10 CHIMERIC PROTEIN
11
12 (iii) NUMBER OF SEQUENCES: 38
13
14 (iv) CORRESPONDENCE ADDRESS:
15 (A) ADDRESSEE: Sim & McBurney
16 (B) STREET: 6th Floor, 330 University Avenue
17 (C) CITY: Toronto
18 (D) STATE: Ontario
19 (E) COUNTRY: Canada
20 (F) ZIP: M5G 1R7
21
22 (v) COMPUTER READABLE FORM:
23 (A) MEDIUM TYPE: Floppy disk
24 (B) COMPUTER: IBM PC compatible
25 (C) OPERATING SYSTEM: PC-DOS/MS-DOS
26 (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
27
28 (vi) CURRENT APPLICATION DATA:
29 (A) APPLICATION NUMBER:
30 (B) FILING DATE:
31 (C) CLASSIFICATION:
32
33 (vii) PRIOR APPLICATION DATA:
34 (A) APPLICATION NUMBER: US 08/467,961
35 (B) FILING DATE: 06-JUN-1995
36
37 (vii) PRIOR APPLICATION DATA:
38 (A) APPLICATION NUMBER: US 08/001,554
39 (B) FILING DATE: 06-JAN-1993
40
41 (vii) PRIOR APPLICATION DATA:
42 (A) APPLICATION NUMBER: GB 9200117.1
43 (B) FILING DATE: 06-JAN-1992
44
45 (viii) ATTORNEY/AGENT INFORMATION:
46 (A) NAME: STEWART, Michael I**ENTERED**

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47 (B) REGISTRATION NUMBER: 24,973
48 (C) REFERENCE/DOCKET NUMBER: 1038-1000 MIS:jb
49
50 (ix) TELECOMMUNICATION INFORMATION:
51 (A) TELEPHONE: (416) 595-1155
52 (B) TELEFAX: (416) 595-1163
53
54
55 (2) INFORMATION FOR SEQ ID NO:1:
56
57 (i) SEQUENCE CHARACTERISTICS:
58 (A) LENGTH: 1844 base pairs
59 (B) TYPE: nucleic acid
60 (C) STRANDEDNESS: single
61 (D) TOPOLOGY: linear
62
63 (ii) MOLECULE TYPE: DNA (genomic)
64
65
66
67 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:
68
69 AAGTCAATAC CAACAACTAT TAGCAGTCAT ACGTGCAAGA ACAAGAAAGA AGAGATTCAA 60
70
71 AAAGCTAAAT AAGAGAAAATC AAAACAAAAG GTATAGAACCA CCCGAACAAC AAAATCAAAA 120
72
73 CATCCAATCC ATTTTAAACA AAAATTCCAA AAGAGACCGG CAACACAAACA AGCACCAAAC 180
74
75 ACAATGCCAA CTTTAATACT GCTAATTATT ACAACAAATGA TTATGGCATC TTCCTGCCAA 240
76
77 ATAGATATCA CAAAACTACA GCATGTAGGT GTATTGGTCA ACAGTCCCAA AGGGATGAAG 300
78
79 ATATCACAAA ACTTCGAAAC AAGATATCTA ATTTGAGCC TCATACCAAA AATAGAAGAC 360
80
81 TCTAACTCTT GTGGTGACCA ACAGATCAAA CAATACAAGA GGTTATTGGA TAGACTGATC 420
82
83 ATCCCTCTAT ATGATGGATT AAGATTACAG AAAGATGTGA TAGTAACCAA TCAAGAATCC 480
84
85 AATGAAAACA CTGATCCCAG AACAAAGACGA TCCTTTGGAG GGGTAATTGG AACCATGCT 540
86
87 CTGGGAGTAG CAACCTCAGC ACAATTACA GCGGCAGTTG CTCTGGTGA AGCCAAGCAG 600
88
89 GCAAAATCAG ACATCGAAAA ACTCAAAGAA GCAATCAGGG ACACAAACAA AGCAGTGCAG 660
90
91 TCAGTTCAGA GCTCTATAGG AAATTAAATA GTAGCAATTA AATCAGTCCA AGATTATGTC 720
92
93 AACAAACGAAA TGGTGCCATC GATTGCTAGA CTAGGTTGTG AAGCAGCAGG ACTTCAATTA 780
94
95 GGAATTGCAT TAACACAGCA TTACTCAGAA TTAACAAACA TATTGGTGA TAACATAGGA 840
96
97 TCGTTACAAG AAAAAGGAAT AAAATTACAA GGTATAGCAT CATTATACCG CACAAATATC 900
98
99 ACAGAAATAT TCACAACATC AACAGTTGAT AAATATGATA TCTATGATCT ATTATTTACA 960

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100	GAATCAATAA AGGTGAGAGT TATAGATGTT GATTGAATG ATTACTCAAT CACCCCTCAA	1020
101	GTCAGACTCC CTTTATTAAC TAGGCTGCTG AACACTCAGA TCTACAAAGT AGATTCCATA	1080
102		
103	TCATATAATA TCCAAAACAG AGAATGGTAT ATCCCTCTTC CCAGCCATAT CATGACGAAA	1140
104		
105	GGGGCATTTC TAGGTGGAGC AGATGTCAAG GAATGTATAG AAGCATTAG CAGTTATATA	1200
106		
107	TGCCCTTCTG ATCCAGGATT TGTACTAAC CATGAAATGG AGAGCTGCTT ATCAGGAAAC	1260
108		
109	ATATCCAAT GTCCAAGAAC CACGGTCACA TCAGACATTG TTCCAAGATA TGCATTTGTC	1320
110		
111	AATGGAGGAG TGGTTGCAAA CTGTATAACA ACCACCTGTA CATGCAACGG AATCGACAAT	1380
112		
113	AGAATCAATC AACCACCTGA TCAAGGAGTA AAAATTATAA CACATAAAGA ATGTAATACA	1440
114		
115	ATAGGTATCA ACGBAATGCT GTTCAATACA AATAAAGAAG GAACTCTTGC ATTCTACACA	1500
116		
117	CTTAACAAAG CCAAATCAGA TCTAGAAGAA TCAAAAGAAT GGATAAGAAG GTCAAATCAA	1560
118		
119	AAACTAGATT CTATTGGAAA CTGGCATCAA TCTAGCACTA CAATCATAAT TATTTTAATA	1680
120		
121	ATGATCATT AATTGTTAT AATTAATGTA ACGATAATTA CAATTGCAAT TAAGTATTAC	1740
122		
123	AGAATTCAAA AGAGAAATCG AGTGGATCAA AATGACAAGC CATATGTACT AACAAACAAA	1800
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125	TGACATATCT ATAGATCATT AGATATTAAA ATTATAAAAA ACTT	1844
126		
127		
128		
129		
130		
131	(2) INFORMATION FOR SEQ ID NO:2:	
132		
133	(i) SEQUENCE CHARACTERISTICS:	
134	(A) LENGTH: 539 amino acids	
135	(B) TYPE: amino acid	
136	(C) STRANDEDNESS: single	
137	(D) TOPOLOGY: linear	
138		
139		
140		
141	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:	
142		
143	Met Pro Thr Leu Ile Leu Leu Ile Ile Thr Thr Met Ile Met Ala Ser	
144	1 5 10 15	
145		
146	Ser Cys Gln Ile Asp Ile Thr Lys Leu Gln His Val Gly Val Leu Val	
147	20 25 30	
148		
149	Asn Ser Pro Lys Gly Met Lys Ile Ser Gln Asn Phe Glu Thr Arg Tyr	
150	35 40 45	
151		
152	Leu Ile Leu Ser Leu Ile Pro Lys Ile Glu Asp Ser Asn Ser Cys Gly	

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153 50 55 60
154
155 Asp Gln Gln Ile Lys Gln Tyr Lys Arg Leu Leu Asp Arg Leu Ile Ile
156 65 70 75 80
157
158 Pro Leu Tyr Asp Gly Leu Arg Leu Gln Lys Asp Val Ile Val Thr Asn
159 85 90 95
160
161 Gln Glu Ser Asn Glu Asn Thr Asp Pro Arg Thr Arg Arg Ser Phe Gly
162 100 105 110
163
164 Gly Val Ile Gly Thr Ile Ala Leu Gly Val Ala Thr Ser Ala Gln Ile
165 115 120 125
166
167 Thr Ala Ala Val Ala Leu Val Glu Ala Lys Gln Ala Lys Ser Asp Ile
168 130 135 140
169
170 Glu Lys Leu Lys Glu Ala Ile Arg Asp Thr Asn Lys Ala Val Gln Ser
171 145 150 155 160
172
173 Val Gln Ser Ser Ile Gly Asn Leu Ile Val Ala Ile Lys Ser Val Gln
174 165 170 175
175
176 Asp Tyr Val Asn Asn Glu Ile Val Pro Ser Ile Ala Arg Leu Gly Cys
177 180 185 190
178
179 Glu Ala Ala Gly Leu Gln Leu Gly Ile Ala Leu Thr Gln His Tyr Ser
180 195 200 205
181
182 Glu Leu Thr Asn Ile Phe Gly Asp Asn Ile Gly Ser Leu Gln Glu Lys
183 210 215 220
184
185 Gly Ile Lys Leu Gln Gly Ile Ala Ser Leu Tyr Arg Thr Asn Ile Thr
186 225 230 235 240
187
188 Glu Ile Phe Thr Thr Ser Thr Val Asp Lys Tyr Asp Ile Tyr Asp Leu
189 245 250 255
190
191 Leu Phe Thr Glu Ser Ile Lys Val Arg Val Ile Asp Val Asp Leu Asn
192 260 265 270
193
194 Asp Tyr Ser Ile Thr Leu Gln Val Arg Leu Pro Leu Leu Thr Arg Leu
195 275 280 285
196
197 Leu Asn Thr Gln Ile Tyr Lys Val Asp Ser Ile Ser Tyr Asn Ile Gln
198 290 295 300
199
200 Asn Arg Glu Trp Tyr Ile Pro Leu Pro Ser His Ile Met Thr Lys Gly
201 305 310 315 320
202
203 Ala Phe Leu Gly Gly Ala Asp Val Lys Glu Cys Ile Glu Ala Phe Ser
204 325 330 335
205

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206 Ser Tyr Ile Cys Pro Ser Asp Pro Gly Phe Val Leu Asn His Glu Met
207 340 345 350
208
209 Glu Ser Cys Leu Ser Gly Asn Ile Ser Gln Cys Pro Arg Thr Thr Val
210 355 360 365
211
212 Thr Ser Asp Ile Val Pro Arg Tyr Ala Phe Val Asn Gly Gly Val Val
213 370 375 380
214
215 Ala Asn Cys Ile Thr Thr Cys Thr Cys Asn Gly Ile Asp Asn Arg
216 385 390 395 400
217
218 Ile Asn Gln Pro Pro Asp Gln Gly Val Lys Ile Ile Thr His Lys Glu
219 405 410 415
220
221 Cys Asn Thr Ile Gly Ile Asn Gly Met Leu Phe Asn Thr Asn Lys Glu
222 420 425 430
223
224 Gly Thr Leu Ala Phe Tyr Thr Pro Asn Asp Ile Thr Leu Asn Asn Ser
225 435 440 445
226
227 Val Ala Leu Asp Pro Ile Asp Ile Ser Ile Glu Leu Asn Lys Ala Lys
228 450 455 460
229
230 Ser Asp Leu Glu Glu Ser Lys Glu Trp Ile Arg Arg Ser Asn Gln Lys
231 465 470 475 480
232
233 Leu Asp Ser Ile Gly Asn Trp His Gln Ser Ser Thr Thr Ile Ile Ile
234 485 490 495
235
236 Ile Leu Ile Met Ile Ile Ile Leu Phe Ile Ile Asn Val Thr Ile Ile
237 500 505 510
238
239 Thr Ile Ala Ile Lys Tyr Tyr Arg Ile Gln Lys Arg Asn Arg Val Asp
240 515 520 525
241
242 Gln Asn Asp Lys Pro Tyr Val Leu Thr Asn Lys
243 530 535
244
245
246 (2) INFORMATION FOR SEQ ID NO:3:
247
248 (i) SEQUENCE CHARACTERISTICS:
249 (A) LENGTH: 1833 base pairs
250 (B) TYPE: nucleic acid
251 (C) STRANDEDNESS: single
252 (D) TOPOLOGY: linear
253
254
255
256 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:
257
258 AGACAAATCC AAATTCGAGA TGGAATACTG GAAGCATACC AATCACGGAA AGGATGCTGG

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**SEQUENCE VERIFICATION REPORT
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Original Text